

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/712,302

1812

DATE: 02/03/98
TIME: 20:36:40

INPUT SET: S23147.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Grotendorst, Gary R.
Bradham Jr., Douglas M.,

(ii) TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Spensley Horn Jubas & Lubitz
(B) STREET: 4225 Executive Square, Suite 1400
(C) CITY: La Jolla
(D) STATE: CA
(E) COUNTRY: US
(F) ZIP: 92037

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/712,302
(B) FILING DATE: 11-SEP-1996
(C) CLASSIFICATION: 435

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/386,680
(B) FILING DATE: 10-FEB-1995

(A) APPLICATION NUMBER: US/08/167,628
(B) FILING DATE:

(A) APPLICATION NUMBER: US/07/752,427
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Wetherell, Jr. Ph.D., John W.
(B) REGISTRATION NUMBER: 31,678
(C) REFERENCE/DOCKET NUMBER: PD-1294

(ix) TELECOMMUNICATION INFORMATION:

ENTERED

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/712,302DATE: 02/03/98
TIME: 20:36:42

INPUT SET: S23147.raw

47 (A) TELEPHONE: 619-455-5100
48 (B) TELEFAX: 619-455-5110
49
50

51 (2) INFORMATION FOR SEQ ID NO:1:
52

53 (i) SEQUENCE CHARACTERISTICS:
54 (A) LENGTH: 2075 base pairs
55 (B) TYPE: nucleic acid
56 (C) STRANDEDNESS: single
57 (D) TOPOLOGY: linear
58

59 (ii) MOLECULE TYPE: cDNA
60
61

62 (vii) IMMEDIATE SOURCE:
63 (B) CLONE: DB60R32
64

65 (ix) FEATURE:
66 (A) NAME/KEY: CDS
67 (B) LOCATION: 130..1177
68
69

70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
71

72	CCCGGCCGAC AGCCCCGAGA CGACAGCCCG GCGCGTCCCG GTCCCCACCT CCGACCACCG	60
73		
74	CCAGCGCTCC AGGCCCCGCG CTCCCCGCTC GCCGCCACCG CGCCCTCCGC TCCGCCCCGCA	120
75		
76	GTGCCAACC ATG ACC GCC GCC AGT ATG GGC CCC GTC CGC GTC GCC TTC	168
77	Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe	
78	1 5 10	
79		
80	GTG GTC CTC CTC GCC CTC TGC AGC CGG CCG GCC GTC GGC CAG AAC TGC	216
81	Val Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys	
82	15 20 25	
83		
84	AGC GGG CCG TGC CGG TGC CCG GAC GAG CCG GCG CCG CGC TGC CCG GCG	264
85	Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala	
86	30 35 40 45	
87		
88	GGC GTG AGC CTC GTG CTG GAC GGC TGC GGC TGC TGC CGC GTC TGC GCC	312
89	Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala	
90	50 55 60	
91		
92	AAG CAG CTG GGC GAG CTG TGC ACC GAG CGC GAC CCC TGC GAC CCG CAC	360
93	Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His	
94	65 70 75	
95		
96	AAG GGC CTC TTC TGT GAC TTC GGC TCC CCG GCC AAC CGC AAG ATC GGC	408
97	Lys Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly	
98	80 85 90	
99		

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100	GTG	TGC	ACC	GCC	AAA	GAT	GGT	GCT	CCC	TGC	ATC	TTC	GGT	GGT	ACG	GTG	456
101	Val	Cys	Thr	Ala	Lys	Asp	Gly	Ala	Pro	Cys	Ile	Phe	Gly	Gly	Thr	Val	
102		95					100					105					
103																	
104	TAC	CGC	AGC	GGA	GAG	TCC	TTC	CAG	AGC	AGC	TGC	AAG	TAC	CAG	TGC	ACG	504
105	Tyr	Arg	Ser	Gly	Glu	Ser	Phe	Gln	Ser	Ser	Cys	Lys	Tyr	Gln	Cys	Thr	
106	110					115					120					125	
107																	
108	TGC	CTG	GAC	GGG	GCG	GTG	GGC	TGC	ATG	CCC	CTG	TGC	AGC	ATG	GAC	GTT	552
109	Cys	Leu	Asp	Gly	Ala	Val	Gly	Cys	Met	Pro	Leu	Cys	Ser	Met	Asp	Val	
110					130					135					140		
111																	
112	CGT	CTG	CCC	AGC	CCT	GAC	TGC	CCC	TTC	CCG	AGG	AGG	GTC	AAG	CTG	CCC	600
113	Arg	Leu	Pro	Ser	Pro	Asp	Cys	Pro	Phe	Pro	Arg	Arg	Val	Lys	Leu	Pro	
114				145					150					155			
115																	
116	GGG	AAA	TGC	TGC	GAG	GAG	TGG	GTG	TGT	GAC	GAG	CCC	AAG	GAC	CAA	ACC	648
117	Gly	Lys	Cys	Cys	Glu	Glu	Trp	Val	Cys	Asp	Glu	Pro	Lys	Asp	Gln	Thr	
118			160					165					170				
119																	
120	GTG	GTT	GGG	CCT	GCC	CTC	GCG	GCT	TAC	CGA	CTG	GAA	GAC	ACG	TTT	GGC	696
121	Val	Val	Gly	Pro	Ala	Leu	Ala	Ala	Tyr	Arg	Leu	Glu	Asp	Thr	Phe	Gly	
122		175					180					185					
123																	
124	CCA	GAC	CCA	ACT	ATG	ATT	AGA	GCC	AAC	TGC	CTG	GTC	CAG	ACC	ACA	GAG	744
125	Pro	Asp	Pro	Thr	Met	Ile	Arg	Ala	Asn	Cys	Leu	Val	Gln	Thr	Thr	Glu	
126	190					195				200						205	
127																	
128	TGG	AGC	GCC	TGT	TCC	AAG	ACC	TGT	GGG	ATG	GGC	ATC	TCC	ACC	CGG	GTT	792
129	Trp	Ser	Ala	Cys	Ser	Lys	Thr	Cys	Gly	Met	Gly	Ile	Ser	Thr	Arg	Val	
130					210					215					220		
131																	
132	ACC	AAT	GAC	AAC	GCC	TCC	TGC	AGG	CTA	GAG	AAG	CAG	AGC	CGC	CTG	TGC	840
133	Thr	Asn	Asp	Asn	Ala	Ser	Cys	Arg	Leu	Glu	Lys	Gln	Ser	Arg	Leu	Cys	
134				225					230					235			
135																	
136	ATG	GTC	AGG	CCT	TGC	GAA	GCT	GAC	CTG	GAA	GAG	AAC	ATT	AAG	AAG	GGC	888
137	Met	Val	Arg	Pro	Cys	Glu	Ala	Asp	Leu	Glu	Glu	Asn	Ile	Lys	Lys	Gly	
138			240					245					250				
139																	
140	AAA	AAG	TGC	ATC	CGT	ACT	CCC	AAA	ATC	TCC	AAG	CCT	ATC	AAG	TTT	GAG	936
141	Lys	Lys	Cys	Ile	Arg	Thr	Pro	Lys	Ile	Ser	Lys	Pro	Ile	Lys	Phe	Glu	
142		255						260				265					
143																	
144	CTT	TCT	GGC	TGC	ACC	AGC	ATG	AAG	ACA	TAC	CGA	GCT	AAA	TTC	TGT	GGA	984
145	Leu	Ser	Gly	Cys	Thr	Ser	Met	Lys	Thr	Tyr	Arg	Ala	Lys	Phe	Cys	Gly	
146	270					275					280					285	
147																	
148	GTA	TGT	ACC	GAC	GGC	CGA	TGC	TGC	ACC	CCC	CAC	AGA	ACC	ACC	ACC	CTG	1032
149	Val	Cys	Thr	Asp	Gly	Arg	Cys	Cys	Thr	Pro	His	Arg	Thr	Thr	Thr	Leu	
150					290					295					300		
151																	
152	CCG	GTG	GAG	TTC	AAG	TGC	CCT	GAC	GGC	GAG	GTC	ATG	AAG	AAG	AAC	ATG	1080

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153	Pro	Val	Glu	Phe	Lys	Cys	Pro	Asp	Gly	Glu	Val	Met	Lys	Lys	Asn	Met	
154				305					310					315			
155																	
156	ATG	TTC	ATC	AAG	ACC	TGT	GCC	TGC	CAT	TAC	AAC	TGT	CCC	GGA	GAC	AAT	1128
157	Met	Phe	Ile	Lys	Thr	Cys	Ala	Cys	His	Tyr	Asn	Cys	Pro	Gly	Asp	Asn	
158			320					325					330				
159																	
160	GAC	ATC	TTT	GAA	TCG	CTG	TAC	TAC	AGG	AAG	ATG	TAC	GGA	GAC	ATG	GCA	T
161	Asp	Ile	Phe	Glu	Ser	Leu	Tyr	Tyr	Arg	Lys	Met	Tyr	Gly	Asp	Met	Ala	1177
162		335					340					345					
163																	
164	GAAGCCAGAG	AGTGAGAGAC	ATTA	ACTCAT	TAGACTGGAA	CTTGAACTGA	TTCACATCTC										1237
165																	
166	ATTTTTC	CGT	AAAAATGATT	TCAGTAGCAC	AAGTTATTTA	AATCTGTTTT	TCTAACTGGG										1297
167																	
168	GGAAAAGATT	CCCACCCAAT	TCAAAACATT	GTGCCATGTC	AAACAAATAG	TCTATCTTCC											1357
169																	
170	CCAGACACTG	GTTTGAAGAA	TGTTAAGACT	TGACAGTGGA	ACTACATTAG	TACACAGCAC											1417
171																	
172	CAGAATGTAT	ATTAAGGTGT	GGCTTTAGGA	GCAGTGGGAG	GGTACCGGCC	CGGTTAGTAT											1477
173																	
174	CATCAGATCG	ACTCTTATAC	GAGTAATATG	CCTGCTATTT	GAAGTGTAAT	TGAGAAGGAA											1537
175																	
176	AATTTTAGCG	TGCTCACTGA	CCTGCCTGTA	GCCCCAGTGA	CAGCTAGGAT	GTGCATTCTC											1597
177																	
178	CAGCCATCAA	GAGACTGAGT	CAAGTTGTTC	CTTAAGTCAG	AACAGCAGAC	TCAGCTCTGA											1657
179																	
180	CATTCTGATT	CGAATGACAC	TGTTCAGGAA	TCGGAATCCT	GTCGATTAGA	CTGGACAGCT											1717
181																	
182	TGTGGCAAGT	GAATTTGCCT	GTAACAAGCC	AGATTTTTTTA	AAATTTATAT	TGTAAATATT											1777
183																	
184	GTGTGTGTGT	GTGTGTGTGT	ATATATATAT	ATATATGTAC	AGTTATCTAA	GTTAATTTAA											1837
185																	
186	AGTTGTTTGT	GCCTTTTTTAT	TTTTGTTTTT	AATGCTTTGA	TATTTCAATG	TTAGCCTCAA											1897
187																	
188	TTTCTGAACA	CCATAGGTAG	AATGTAAAGC	TTGTCTGATC	GTTCAAAGCA	TGAAATGGAT											1957
189																	
190	ACTTATATGG	AAATTCTGCT	CAGATAGAAT	GACAGTCCGT	CAAAACAGAT	TGTTTGCAAA											2017
191																	
192	GGGGAGGCAT	CAGTGTCTTG	GCAGGCTGAT	TTCTAGGTAG	GAAATGTGGT	AGCTCACG											2075
193																	
194																	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 349 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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206	Met	Thr	Ala	Ala	Ser	Met	Gly	Pro	Val	Arg	Val	Ala	Phe	Val	Val	Leu
207	1				5					10					15	
208																
209	Leu	Ala	Leu	Cys	Ser	Arg	Pro	Ala	Val	Gly	Gln	Asn	Cys	Ser	Gly	Pro
210				20					25					30		
211																
212	Cys	Arg	Cys	Pro	Asp	Glu	Pro	Ala	Pro	Arg	Cys	Pro	Ala	Gly	Val	Ser
213			35					40					45			
214																
215	Leu	Val	Leu	Asp	Gly	Cys	Gly	Cys	Cys	Arg	Val	Cys	Ala	Lys	Gln	Leu
216		50					55					60				
217																
218	Gly	Glu	Leu	Cys	Thr	Glu	Arg	Asp	Pro	Cys	Asp	Pro	His	Lys	Gly	Leu
219	65					70					75					80
220																
221	Phe	Cys	Asp	Phe	Gly	Ser	Pro	Ala	Asn	Arg	Lys	Ile	Gly	Val	Cys	Thr
222					85					90					95	
223																
224	Ala	Lys	Asp	Gly	Ala	Pro	Cys	Ile	Phe	Gly	Gly	Thr	Val	Tyr	Arg	Ser
225				100					105					110		
226																
227	Gly	Glu	Ser	Phe	Gln	Ser	Ser	Cys	Lys	Tyr	Gln	Cys	Thr	Cys	Leu	Asp
228			115					120					125			
229																
230	Gly	Ala	Val	Gly	Cys	Met	Pro	Leu	Cys	Ser	Met	Asp	Val	Arg	Leu	Pro
231		130					135					140				
232																
233	Ser	Pro	Asp	Cys	Pro	Phe	Pro	Arg	Arg	Val	Lys	Leu	Pro	Gly	Lys	Cys
234	145					150					155					160
235																
236	Cys	Glu	Glu	Trp	Val	Cys	Asp	Glu	Pro	Lys	Asp	Gln	Thr	Val	Val	Gly
237					165					170					175	
238																
239	Pro	Ala	Leu	Ala	Ala	Tyr	Arg	Leu	Glu	Asp	Thr	Phe	Gly	Pro	Asp	Pro
240				180					185					190		
241																
242	Thr	Met	Ile	Arg	Ala	Asn	Cys	Leu	Val	Gln	Thr	Thr	Glu	Trp	Ser	Ala
243			195					200					205			
244																
245	Cys	Ser	Lys	Thr	Cys	Gly	Met	Gly	Ile	Ser	Thr	Arg	Val	Thr	Asn	Asp
246		210					215					220				
247																
248	Asn	Ala	Ser	Cys	Arg	Leu	Glu	Lys	Gln	Ser	Arg	Leu	Cys	Met	Val	Arg
249	225					230					235					240
250																
251	Pro	Cys	Glu	Ala	Asp	Leu	Glu	Glu	Asn	Ile	Lys	Lys	Gly	Lys	Lys	Cys
252					245					250					255	
253																
254	Ile	Arg	Thr	Pro	Lys	Ile	Ser	Lys	Pro	Ile	Lys	Phe	Glu	Leu	Ser	Gly
255				260					265					270		
256																
257	Cys	Thr	Ser	Met	Lys	Thr	Tyr	Arg	Ala	Lys	Phe	Cys	Gly	Val	Cys	Thr
258			275					280					285			

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SEQUENCE VERIFICATION REPORT
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